

# SEQUENCE LISTING

<110> Applicant:  
Taylor, Garry  
Portner, Allen  
Takimoto, Toru  
Babu, Y. Sudhakar  
Rowland, R. Scott

<120> Title of Invention: Three Dimensional Structure of Paramyxovirus Hemagglutinin-Neuraminidases and Use Thereof

<130> File Reference: 1663/00142

<160> Number of SEQ ID Nos.: 1

<210> SEQ ID NO:#1

<211> LENGTH: 577 amino acids

<212> TYPE: protein

<213> Organism: Newcastle Disease Virus Hemagglutinin-Neuraminidase (Kansas Strain)

<223> STRANDEDNESS: single  
TOPOLOGY: linear

<400> SEQUENCE:

1 mdravsqval endereaknt wrlifriail lltvvtlats vaslvysmga stpsdlvgip  
61 trisraeeki tsalgsnqdv vdriyqkval esplallnte ttimnaitsl syqingaann  
121 sgwgapihdp dfiggigkel ivdnasdvts fypsafqehl nfipapttgs gctripsfdm  
181 sathycytn vilsgcrdhs hshqylalgv lrttatgrif fstlrsisl dtqnkrkscsv  
241 satplgcdml cskvteteee dynsavptlm ahgrlgfdgq yhekdlvtt lfedwvanyp  
301 gvvgggsfidg rvwfsvyggl kpnspsdtvq egkyviykry ndtcpdeqdy qirmakssyk  
361 pgrfggkriq qailsikvst slgedpvlv ppntvtlmga egriltvgts hflyqrgssy  
421 fspallypmt vsnktatlhs pytfnafrp gsipcqasar cpnscvtgvy tdpyplyfyr  
481 nhtlrgvfgt mldseqarln pasavfdsts rsritrvsss stkaayttst cfkvvktkt  
541 yclsiaeisn tlfgefripv llveilkn dg vrearsg

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<130> 1663/00142

<160> 1

<210> 1

<211> 577

<212> PRT

<213> Newcastle Disease Virus (Kansas Strain)

<400> 1

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Ala	Lys	Asn	Thr	trp	Arg	Leu	Ile	Phe	Arg	Ile	Ala	Ile	Leu	Leu	Leu
			20					25					30		
Thr	Val	Val	Thr	Leu	Ala	Thr	Ser	Val	Ala	Ser	Leu	Val	Tyr	Ser	Met
		35					40					45			
Gly	Ala	Ser	Thr	Pro	Ser	Asp	Leu	Val	Gly	Ile	Pro	Thr	Arg	Ile	Ser
	50					55					60				
Arg	Ala	Glu	Glu	Lys	Ile	Thr	Ser	Ala	Leu	Gly	Ser	Asn	Gln	Asp	Val
65					70					75					80
Val	Asp	Arg	Ile	Tyr	Lys	Gln	Val	Ala	Leu	Glu	Ser	Pro	Leu	Ala	Leu
				85					90					95	
Leu	Asn	Thr	Glu	Thr	Thr	Ile	Met	Asn	Ala	Ile	Thr	Ser	Leu	Ser	Tyr
			100					105					110		
Gln	Ile	Asn	Gly	Ala	Ala	Asn	Asn	Ser	Gly	trp	Gly	Ala	Pro	Ile	His
		115					120					125			
Asp	Pro	Asp	Phe	Ile	Gly	Gly	Ile	Gly	Lys	Glu	Leu	Ile	Val	Asp	Asn
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Ala	Ser	Asp	Val	Thr	Ser	Phe	Tyr	Pro	Ser	Ala	Phe	Gln	Glu	His	Leu
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Asn	Phe	Ile	Pro	Ala	Pro	Thr	Thr	Gly	Ser	Gly	Cys	Thr	Arg	Ile	Pro
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Ser	Phe	Asp	Met	Ser	Ala	Thr	His	Tyr	Cys	Tyr	Thr	His	Asn	Val	Ile
			180					185					190		
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Gly	Val 210	Leu	Arg	Thr	Thr	Ala 215	Thr	Gly	Arg	Ile	Phe 220	Phe	Ser	Thr	Leu
Arg 225	Ser	Ile	Ser	Leu	Asp 230	Asp	Thr	Gln	Asn	Arg 235	Lys	Ser	Cys	Ser	Val 240
Ser	Ala	Thr	Pro	Leu 245	Gly	Cys	Asp	Met	Leu 250	Cys	Ser	Lys	Val	Thr 255	Glu
Thr	Glu	Glu	Glu 260	Asp	Tyr	Asn	Ser	Ala 265	Val	Pro	Thr	Leu	Met 270	Ala	His
Gly	Arg	Leu 275	Gly	Phe	Asp	Gly	Gln 280	Tyr	His	Glu	Lys	Asp 285	Leu	Asp	Val
Thr	Thr 290	Leu	Phe	Glu	Asp	trp 295	Val	Ala	Asn	Tyr	Pro 300	Gly	Val	Gly	Gly
Gly 305	Ser	Phe	Ile	Asp	Gly 310	Arg	Val	trp	Phe	Ser 315	Val	Tyr	Gly	Gly	Leu 320
Lys	Pro	Asn	Ser	Pro 325	Ser	Asp	Thr	Val	Gln 330	Glu	Gly	Lys	Tyr	Val 335	Ile
Tyr	Lys	Arg	Tyr 340	Asn	Asp	Thr	Cys	Pro 345	Asp	Glu	Gln	Asp	Tyr 350	Gln	Ile
Arg	Met	Ala 355	Lys	Ser	Ser	Tyr	Lys 360	Pro	Gly	Arg	Phe	Gly 365	Gly	Lys	Arg
Ile	Gln 370	Gln	Ala	Ile	Leu	Ser 375	Ile	Lys	Val	Ser	Thr 380	Ser	Leu	Gly	Glu
Asp 385	Pro	Val	Leu	Thr	Val 390	Pro	Pro	Asn	Thr	Val 395	Thr	Leu	Met	Gly	Ala 400
Glu	Gly	Arg	Ile	Leu 405	Thr	Val	Gly	Thr	Ser 410	His	Phe	Leu	Tyr	Gln 415	Arg
Gly	Ser	Ser	Tyr 420	Phe	Ser	Pro	Ala	Leu 425	Leu	Tyr	Pro	Met	Thr 430	Val	Ser
Asn	Lys	Thr 435	Ala	Thr	Leu	His	Ser 440	Pro	Tyr	Thr	Phe	Asn 445	Ala	Phe	Thr
Arg	Pro 450	Gly	Ser	Ile	Pro	Cys 455	Gln	Ala	Ser	Ala	Arg 460	Cys	Pro	Asn	Ser
Cys 465	Val	Thr	Gly	Val	Tyr 470	Thr	Asp	Pro	Tyr	Pro 475	Leu	Ile	Phe	Tyr	Arg 480
Asn	His	Thr	Leu	Arg 485	Gly	Val	Phe	Gly	Thr 490	Met	Leu	Asp	Ser	Glu 495	Gln
Ala	Arg	Leu	Asn 500	Pro	Ala	Ser	Ala	Val 505	Phe	Asp	Ser	Thr	Ser 510	Arg	Ser
Arg	Ile	Thr 515	Arg	Val	Ser	Ser	Ser 520	Ser	Thr	Lys	Ala	Ala 525	Tyr	Thr	Thr

Ser Thr Cys Phe Lys Val Val Lys Thr Asn Lys Thr Tyr Cys Leu Ser  
530 535 540

Ile Ala Glu Ile Ser Asn Thr Leu Phe Gly Glu Phe Arg Ile Val Pro  
545 550 555 560

Leu Leu Val Glu Ile Leu Lys Asn Asp Gly Val Arg Glu Ala Arg Ser  
565 570 575

Gly